```
    1                                M   A   P   L   C   P   S   P   W   L   P   L      12
    1   ACA GTC AGC CGC ATG GCT CCC CTG TGC CCC AGC CCC TGG CTC CCT CTG                  48

   13   L   I   P   A   P   A   P   G   L   T   V   Q   L   L   L   S      28
   49   TTG ATC CCG GCC CCT GCT CCA GGC CTC ACT GTG CAA CTG CTG CTG TCA      96

   29   L   L   L   L   M   P   V   H   P   Q   R   L   P   R   M   Q      44
   97   CTG CTG CTT CTG ATG CCT GTC CAT CCC CAG AGG TTG CCC CGG ATG CAG     144

   45   E   D   S   P   L   G   G   G   S   S   G   E   D   D   P   L      60
  145   GAG GAT TCC CCC TTG GGA GGA GGC TCT TCT GGG GAA GAT GAC CCA CTG     192

   61   G   E   K   D   L   P   S   E   K   D   S   P   R   E   K   D      76
  193   GGC GAG GAG GAT CTG CCC AGT GAA GAG GAT TCA CCC AGA GAG GAG GAT     240

   77   P   P   G   E   E   D   L   P   G   E   E   D   L   P   G   E      92
  241   CCA CCC GGA GAG GAG GAT CTA CCT GGA GAG GAG GAT CTA CCT GGA GAG     288

   93   E   D   L   P   E   V   K   P   K   S   E   E   E   G   S   L     108
  289   GAG GAT CTA CCT GAA GTT AAG CCT AAA TCA GAA GAA GAG GGC TCC CTG     336

  109   K   L   E   D   L   P   T   V   E   A   P   G   D   P   Q   E     124
  337   AAG TTA GAG GAT CTA CCT ACT GTT GAG GCT CCT GGA GAT CCT CAA GAA     384

  125   P   Q   N   N   A   H   R   D   K   E   G   D   D   Q   S   H     140
  385   CCC CAG AAT AAT GCC CAC AGG GAC AAA GAA GGG GAT GAC CAG AGT CAT     432

  141   W   R   Y   G   G   D   P   P   W   P   R   V   S   P   A   C     156
  433   TGG CGC TAT GGA GGC GAC CCG CCC TGG CCC CGG GTG TCC CCA GCC TGC     480

  157   A   G   R   F   Q   S   P   V   D   I   R   P   Q   L   A   A     172
  481   GCG GGC CGC TTC CAG TCC CCG GTG GAT ATC CGC CCC CAG CTC GCC GCC     528

  173   F   C   P   A   L   R   P   L   E   L   L   G   F   Q   L   P     188
  529   TTC TGC CCG GCC CTG CGC CCC CTG GAA CTC CTG GGC TTC CAG CTC CCG     576

  189   P   L   P   E   L   R   L   R   N   N   G   H   S   V   Q   L     204
  577   CCG CTC CCA GAA CTG CGC CTG CGC AAC AAT GGC CAC AGT GTG CAA CTG     624

  205   T   L   P   P   G   L   E   M   A   L   G   P   G   R   E   Y     220
  625   ACC CTG CCT CCT GGG CTA GAG ATG GCT CTG GGT CCC GGG CGG GAG TAC     672

  221   R   A   L   Q   L   H   L   H   W   G   A   A   G   R   P   G     236
  673   CGG GCT CTG CAG CTG CAT CTG CAC TGG GGG GCT GCA GGT CGT CCG GGC     720

  237   S   E   H   T   V   E   G   H   R   F   P   A   E   I   H   V     252
  721   TCG GAG CAC ACT GTG GAA GGC CAC CGT TTC CCT GCC GAG ATC CAC GTG     768

  253   V   H   L   S   T   A   F   A   R   V   D   E   A   L   G   R     268
  769   GTT CAC CTC AGC ACC GCC TTT GCC AGA GTT GAC GAG GCC TTG GGG CGC     816

  269   P   G   G   L   A   V   L   A   A   F   L   E   E   G   P   E     284
  817   CCG GGA GGC CTG GCC GTG TTG GCC GCC TTT CTG GAG GAG GGC CCG GAA     864

  285   E   N   S   A   Y   E   Q   L   L   S   R   L   E   K   I   A     300
  865   GAA AAC AGT GCC TAT GAG CAG TTG CTG TCT CGC TTG GAA GAA ATC GCT     912

  301   K   E   G   S   E   T   Q   V   P   G   L   D   I   S   A   L     316
  913   GAG GAA GGC TCA GAG ACT CAG GTC CCA GGA CTG GAC ATA TCT GCA CTC     960

  317   L   P   S   D   F   S   R   Y   F   Q   Y   E   G   S   L   T     332
  961   CTG CCC TCT GAC TTC AGC CGC TAC TTC CAA TAT GAG GGG TCT CTG ACT    1008

  333   T   P   P   C   A   Q   G   V   I   W   T   V   F   N   Q   T     348
 1009   ACA CCG CCC TGT GCC CAG GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA    1056

  349   V   M   L   S   A   K   Q   L   H   T   L   E   D   T   L   W     364
 1057   GTG ATG CTG AGT GCT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG    1104

  365   G   P   G   D   S   R   L   Q   L   N   F   R   A   T   Q   P     380
 1105   GGA CCT GGT GAC TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT    1152

  381   L   N   G   R   V   I   E   A   S   F   P   A   G   V   D   S     396
 1153   TTG AAT GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC    1200

  397   S   P   R   A   A   E   P   V   Q   L   N   S   C   L   A   A     412
 1201   AGT CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT    1248

  413   G   D   I   L   A   L   V   F   G   L   L   F   A   V   T   S     428
 1249   GGT GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC AGC    1296

  429   V   A   F   L   V   Q   M   R   R   Q   H   R   R   G   T   K     444
 1297   GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA ACC AAA    1344

  445   G   G   V   S   Y   R   P   A   E   V   A   E   T   G   A   *     460
 1345   GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT GGA GCC TAG    1392

 1393   AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA GGC ATC TGA GGG    1440
 1441   GGA GCC GGT AAC TGT CCT GTC CTG CTC ATT ATG CCA CTT CCT TTT AAC    1488
 1489   TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA TAA T                     1522
0
```

FIG. 1

A B

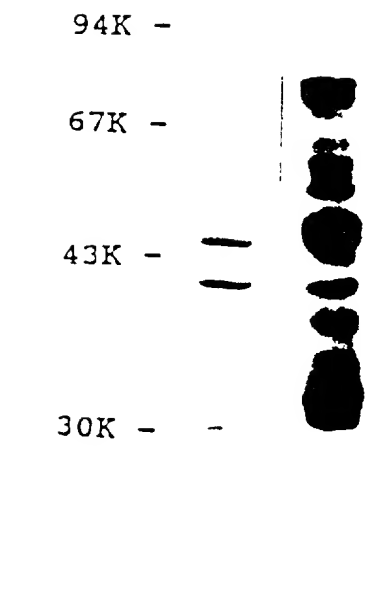


FIG. 2.

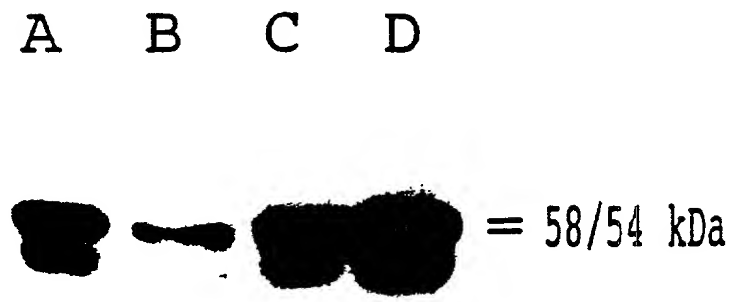


FIG. 3.

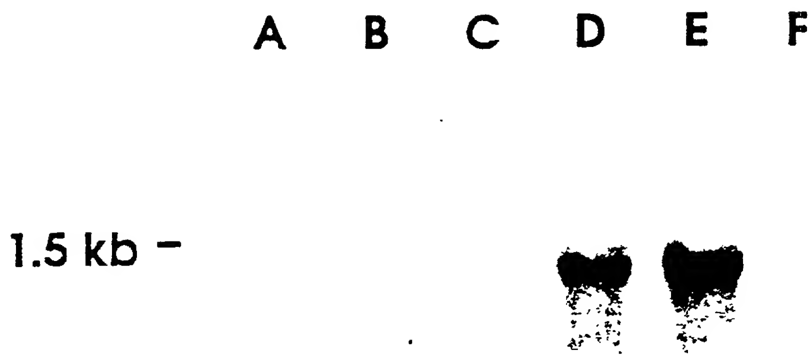


FIG. 4.

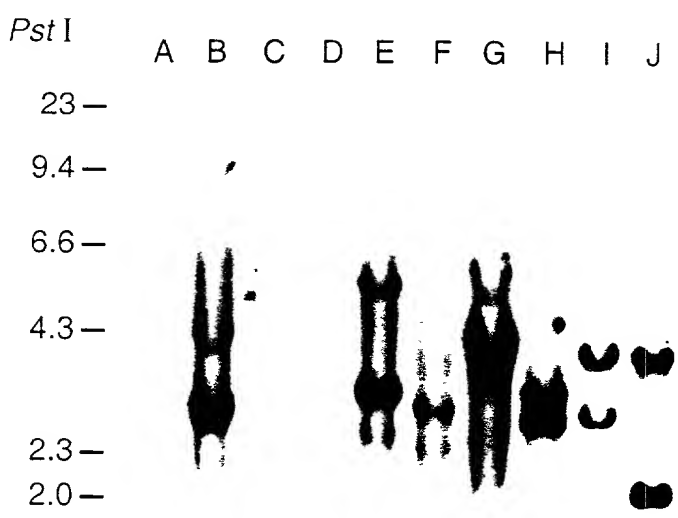


FIG._5

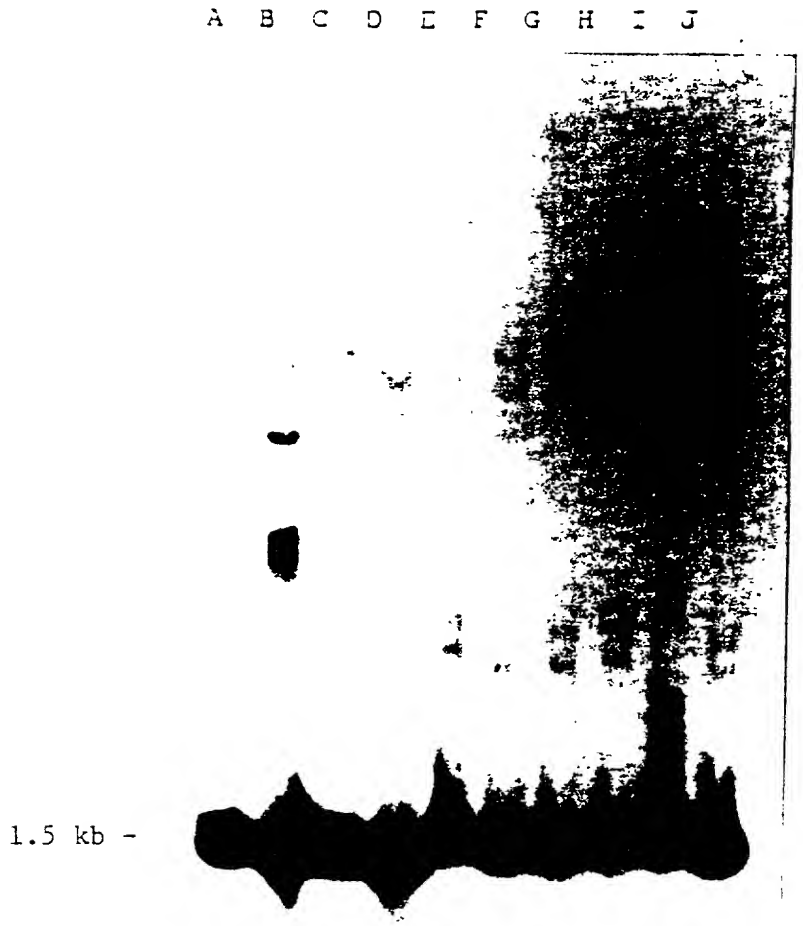
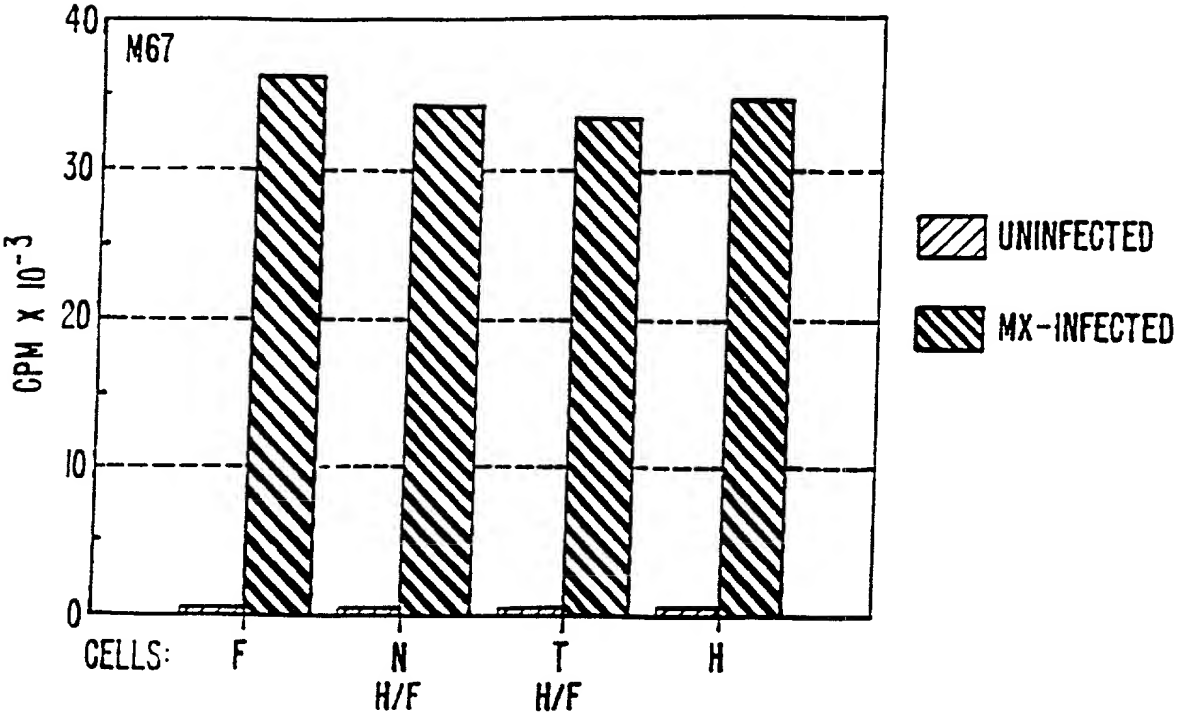


FIG. 5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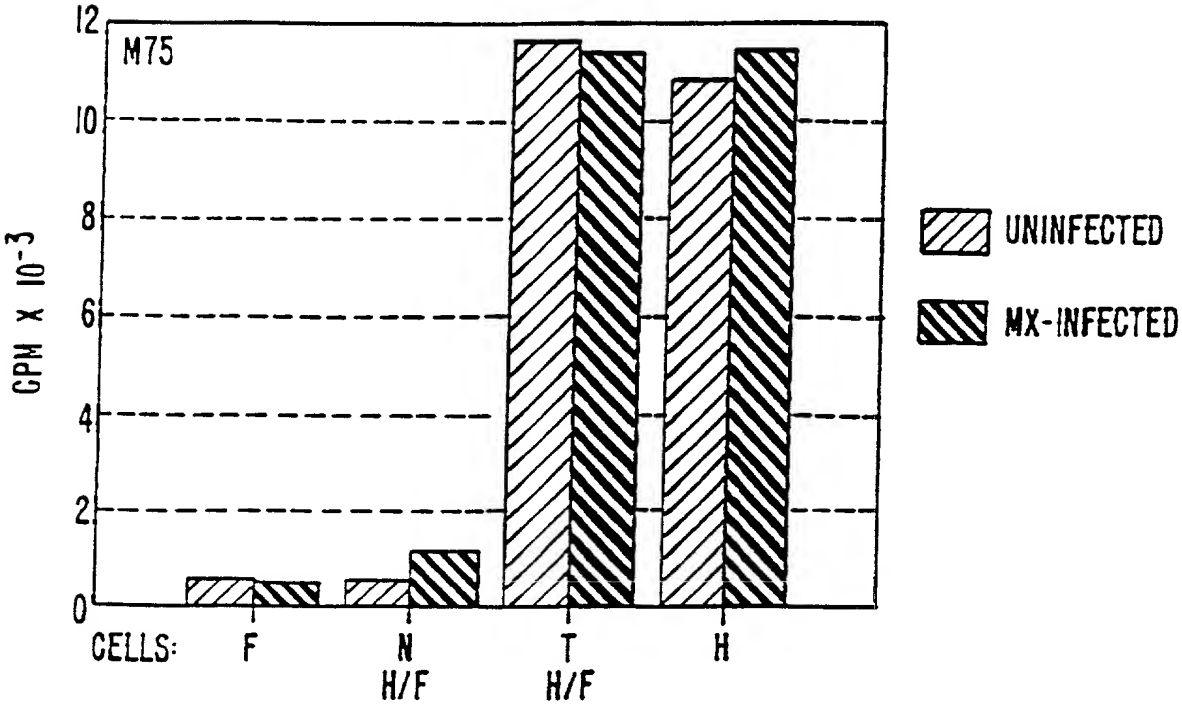
30
20
10
0
CPM X 10-3
CELLS:
F
N
H/F
T
H/F
H
UNINFECTED
MX-INFECTED

FIG. 6A.


M75
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8
6
4
2
0
CPM X 10-3
CELLS:
F
N
H/F
T
H/F
H
UNINFECTED
MX-INFECTED

FIG. 6B.

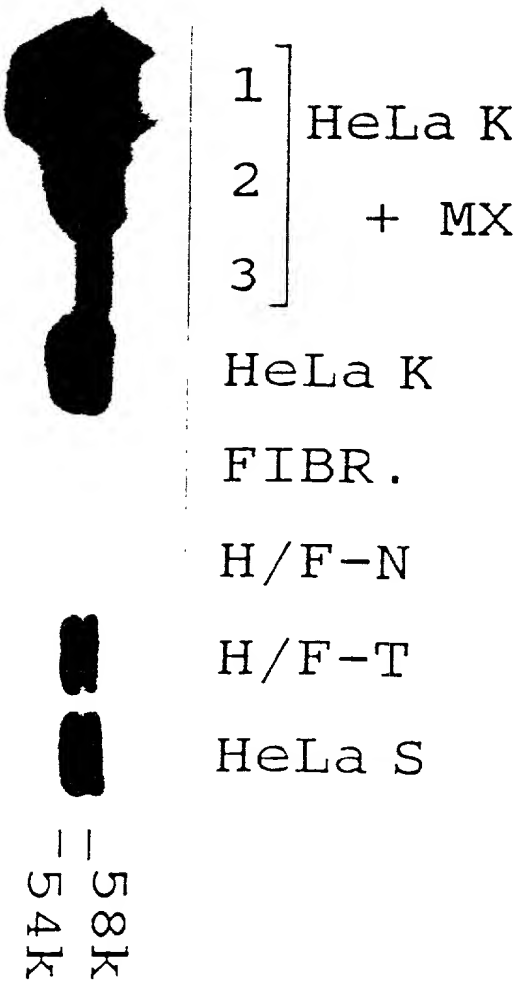

FIG. 7.

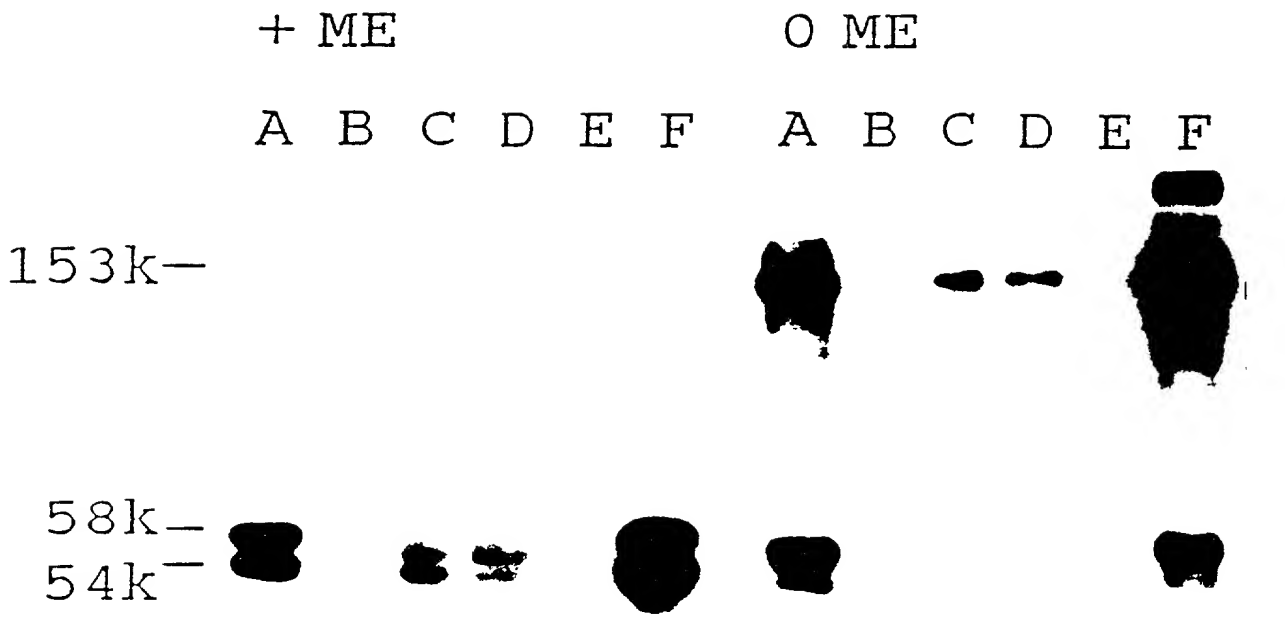

FIG. 8

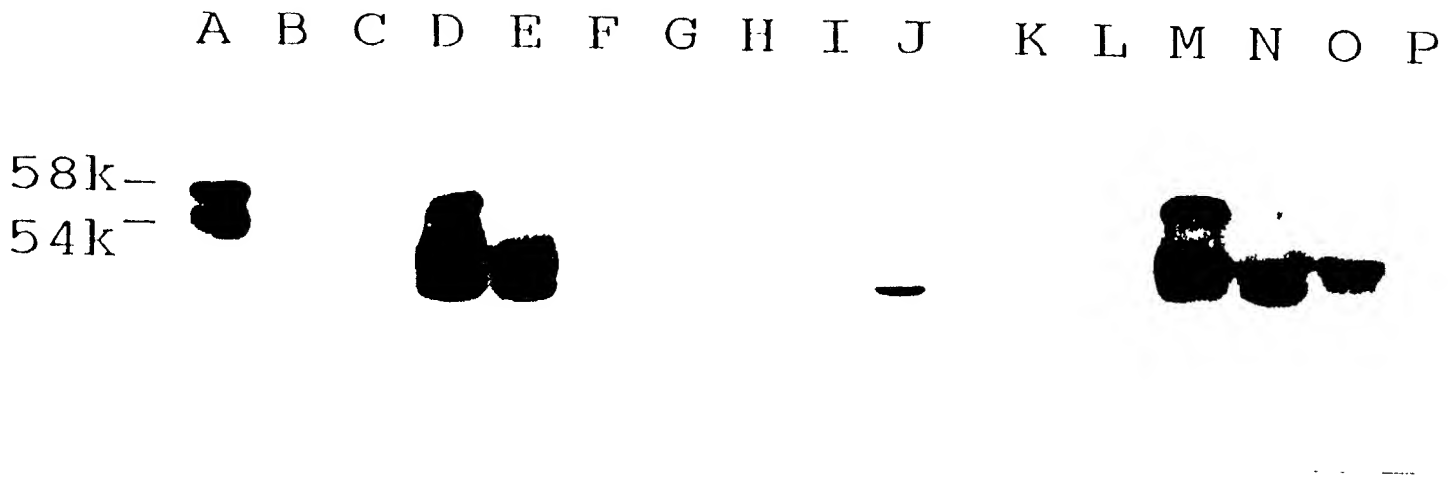

FIG. 9.

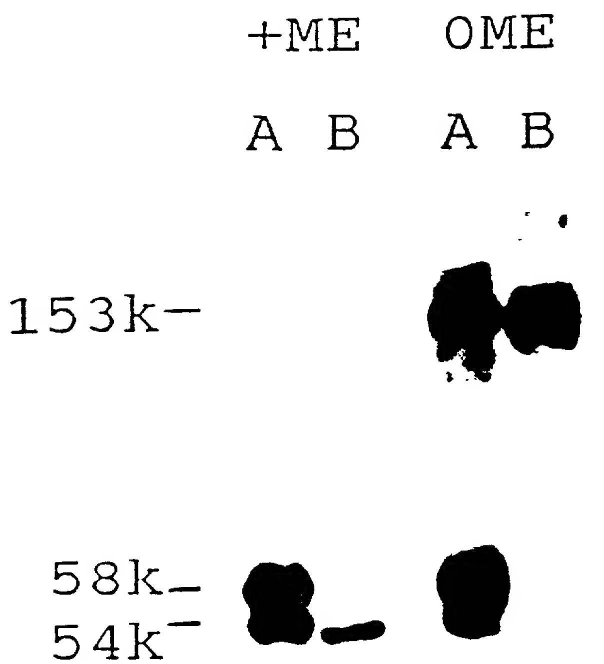

FIG. 10.

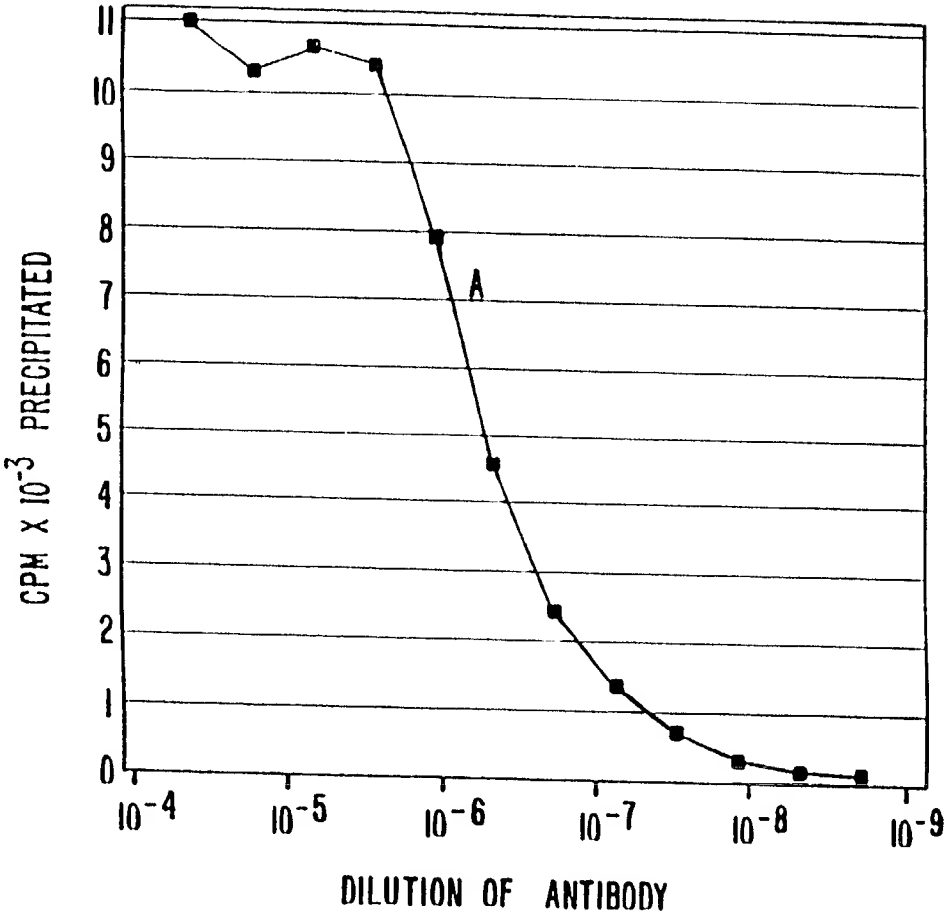

FIG. 11A.

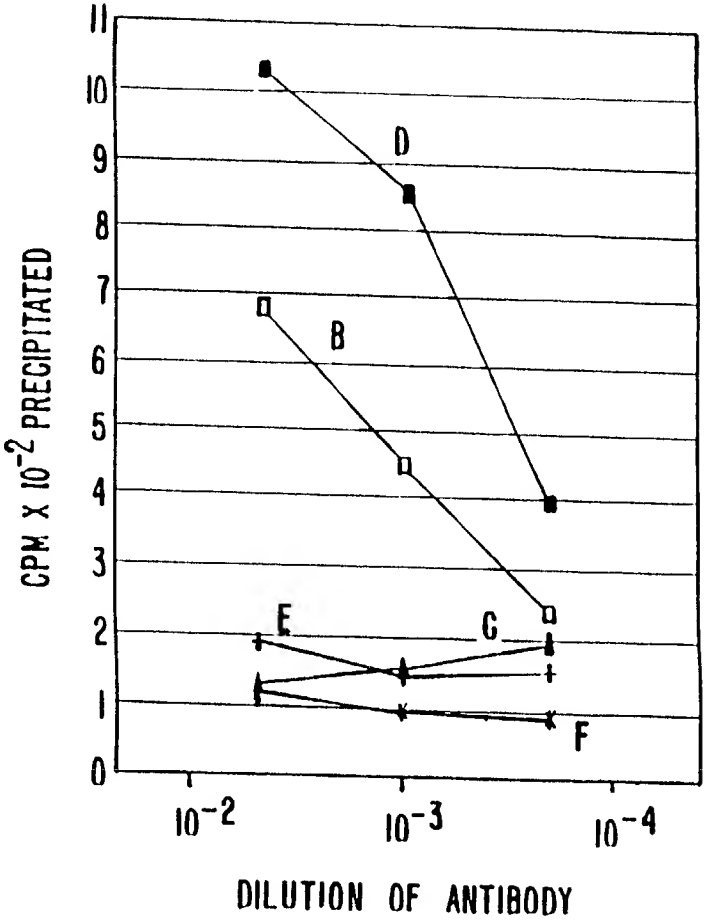

FIG. 11B.

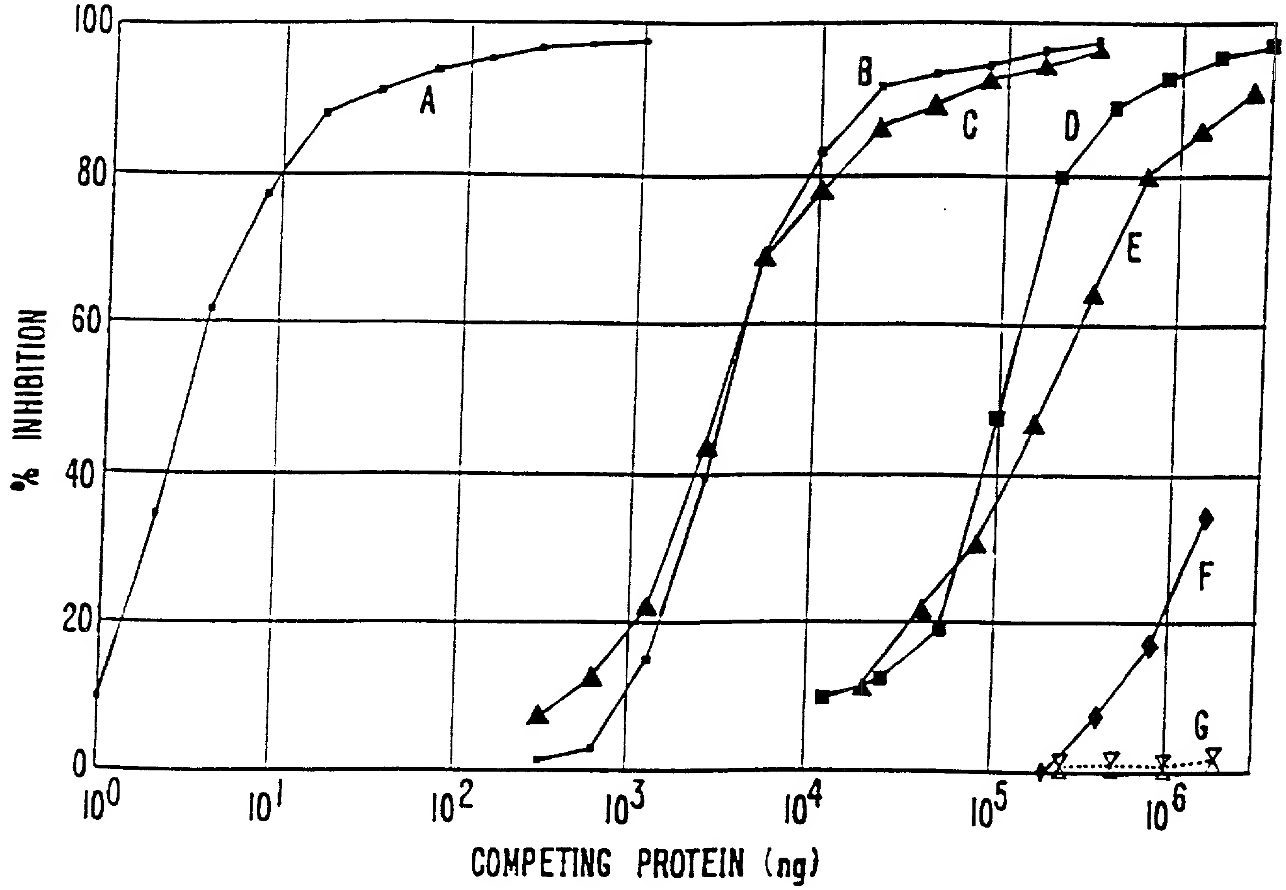
% INHIBITION
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
10^5
10^6
COMPETING PROTEIN (ng)
A
B
C
D
E
F
G

FIG. 12.

FIG. 13A.

FIG. 13B.

FIG. 13C.

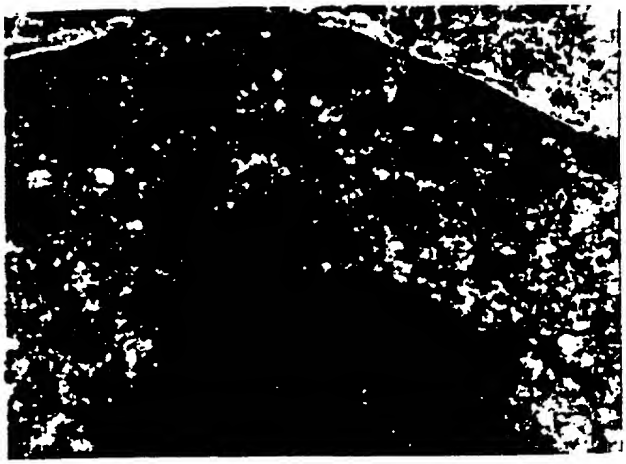

FIG. 13D.

FIG. 13E.

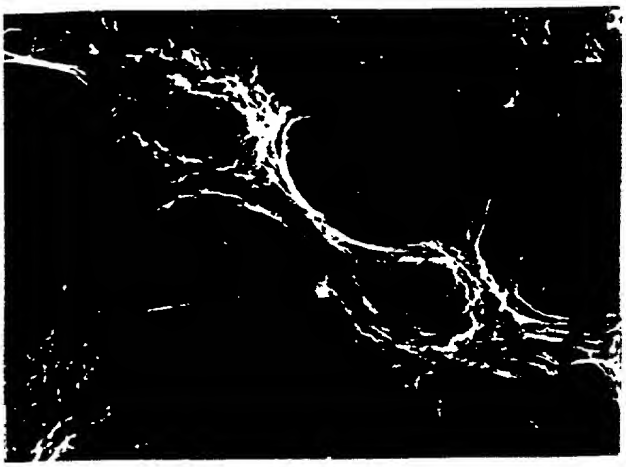

FIG. 13F.

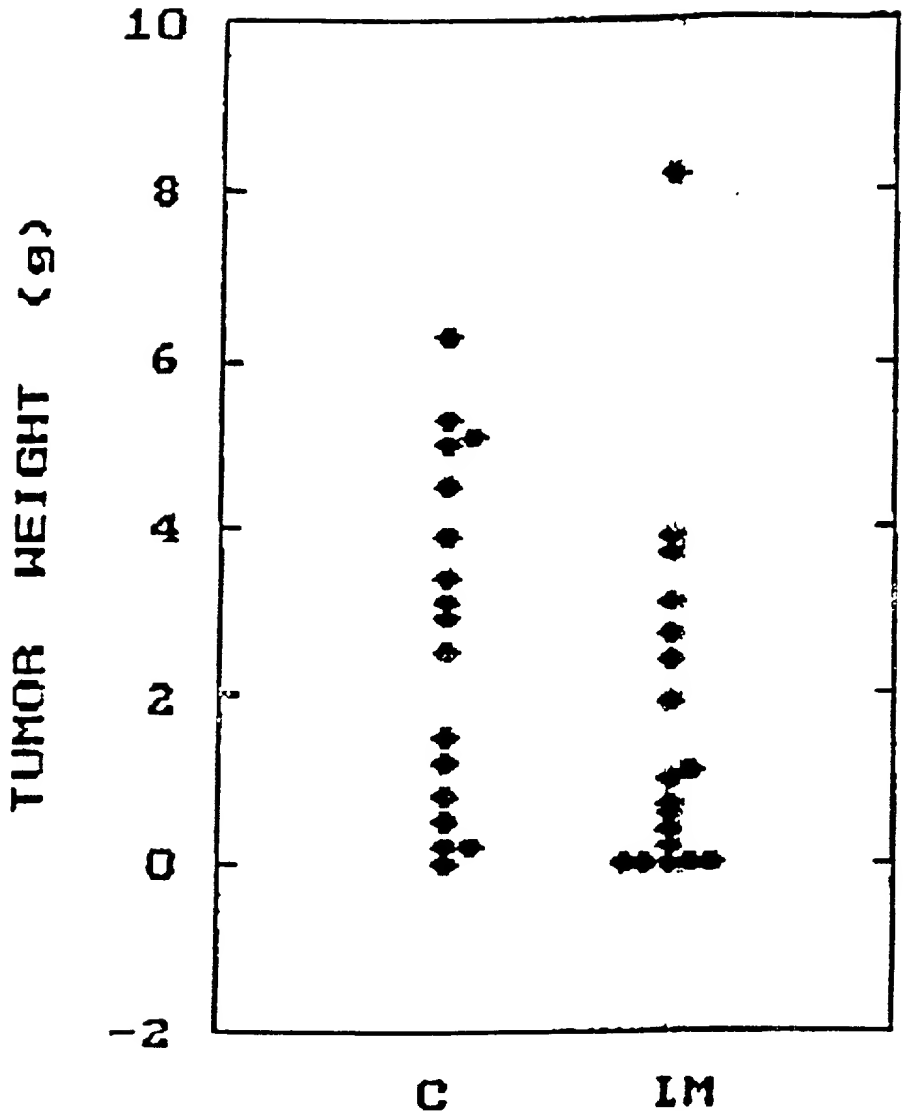

FIG. 14

```
   1 ggatcctgtt gactcgtgac cttaccccca accctgtgct ctctgaaaca tgagctgtgt
  61 ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg
 121 aaggcagcat gctcgttaag agtcatcacc aatccctaat ctcaagtaat cagggacaca
 181 aacactgcgg aaggccgcag ggtcctctgc ctaggaaaac cagagacctt tgttcacttg
 241 tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatcccctt ctgtgagaaa
 301 cacccaagaa ttatcaataa aaaaataaat ttaaaaaaaa aatacaaaaa aaaaaaaaaa
 361 aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta
 421 aatgatcata ttcaaaacca gacggccatc atcacagctc aagtctacct gatttgatct
 481 ctttatcatt gtcattcttt ggattcacta gattagtcat catcctcaaa attctccccc
 541 aagttctaat tacgttccaa acatttaggg gttacatgaa gcttgaacct actaccttct
 601 ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa
 661 tttaaacttt acctctaagt cagttgggta gcctttggct tatttttgta gctaattttg
 721 tagttaatgg atgcactgtg aatcttgcta tgatagtttt cctccacact ttgccactag
 781 gggtaggtag gtactcagtt ttcagtaatt gcttacctaa gaccctaagc cctatttctc
 841 ttgtactggc ctttatctgt aatatgggca tatttaatac aatataattt ttggagtttt
 901 tttgtttgtt tgtttgtttg ttttttttgag acggagtctt gcatctgtca tgcccaggct
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1081 ttttttgtat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc
1141 ctgacttcgt gatccacccg cctcggcctc ccaaagttct gggattacag gtgtgagcca
1201 ccgcacctgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac
1261 tatggtacat ttccttttat taatgtggtg ctgacggtca tataggttct tttgagtttg
1321 gcatgcatat gctacttttt gcagtccttt cattacattt ttctctcttc atttgaagag
1381 catgttatat cttttagctt cacttggctt aaaaggttct ctcattagcc taacacagtg
1441 tcattgttgg taccacttgg atcataagtg gaaaaacagt caagaaattg cacagtaata
1501 cttgtttgta agagggatga ttcaggtgaa tctgacacta agaaactccc ctacctgagg
1561 tctgagattc ctctgacatt gctgtatata ggcttttcct ttgacagcct gtgactgcgg
1621 actatttttc ttaagcaaga tatgctaaag ttttgtgagc ctttttccag agagaggtct
1681 catatctgca tcaagtgaga acatataatg tctgcatgtt tccatatttc aggaatgttt
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2881 agtacacaat gtgcatatcg tggcaggcag tggggagcca atgaaggctt ttgagcagga
2941 gagtaatgtg ttgaaaaata aatataggtt aaacctatca gagcccctct gacacataca
3001 cttgcttttc attcaagctc aagtttgtct cccacatacc cattacttaa ctcaccctcg
```

FIG. 15a

3061 ggctccccta gcagcctgcc ctacctcttt acctgcttcc tggtggagtc agggatgtat
3121 acatgagctg ctttccctct cagccagagg acatgggggg ccccagctcc cctgcctttc
3181 cccttctgtg cctggagctg ggaagcaggc cagggttagc tgaggctggc tggcaagcag
3241 ctgggtggtg ccagggagag cctgcatagt gccaggtggt gccttgggtt ccaagctagt
3301 ccatggcccc gataaccttc tgcctgtgca cacacctgcc cctcactcca cccccatcct
3361 agctttggta tgggggagag ggcacagggc cagacaaacc tgtgagactt tggctccatc
3421 tctgcaaaag ggcgctctgt gagtcagcct gctcccctcc aggcttgctc ctcccccacc
3481 cagctctcgt ttccaatgca cgtacagccc gtacacaccg tgtgctggga cacccc**ACAG**
3541 **TCAGCCGCAT GGCTCCCCTG TGCCCCAGCC CCTGGCTCCC TCTGTTGATC CCGGCCCCTG**
3601 **CTCCAGGCCT CACTGTGCAA CTGCTGCTGT CACTGCTGCT TCTGGTGCCT GTCCATCCCC**
3661 **AGAGGTTGCC CCGGATGCAG GAGGATTCCC CCTTGGGAGG AGGCTCTTCT GGGGAAGATG**
3721 **ACCCACTGGG CGAGGAGGAT CTGCCCAGTG AAGAGGATTC ACCCAGAGAG GAGGATCCAC**
3781 **CCGGAGAGGA GGATCTACCT GGAGAGGAGG ATCTACCTGG AGAGGAGGAT CTACCTGAAG**
3841 **TTAAGCCTAA ATCAGAAGAA GAGGGCTCCC TGAAGTTAGA GGATCTACCT ACTGTTGAGG**
3901 **CTCCTGGAGA TCCTCAAGAA CCCCAGAATA ATGCCCACAG GGACAAAGAA Ggtaagtggt**
3961 catcaatctc caaatccagg ttccaggagg ttcatgactc ccctcccata ccccagccta
4021 ggctctgttc actcagggaa ggaggggaga ctgtactccc cacagaagcc cttccagagg
4081 tcccatacca atatccccat ccccactctc ggaggtagaa agggacagat gtggagagaa
4141 aataaaaagg gtgcaaaagg agagaggtga gctggatgag atgggagaga agggggaggc
4201 tggagaagag aaagggatga gaactgcaga tgagagaaaa aatgtgcaga cagaggaaaa
4261 aaataggtgg agaaggagag tcagagagtt tgaggggaag agaaaaggaa agcttgggag
4321 gtgaagtggg taccagagac aagcaagaag agctggtaga agtcatctca tcttaggcta
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4621 caggctggag tgcaatggcg cgatctcggc tcactgcaac ctccacctcc cgggttcaag
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5761 CACACTGTGG AAGGCCACCG TTTCCCTGCC GAGgtgagcg cggactggcc gagaaggggc
5821 aaaggagcgg ggcggacggg ggccagagac gtggccctct cctaccctcg tgtccttttc
5881 agATCCACGT GGTTCACCTC AGCACCGCCT TTGCCAGAGT TGACGAGGCC TTGGGGCGCC
5941 CGGGAGGCCT GGCCGTGTTG GCCGCCTTTC TGGAGgtacc agatcctgga caccccctac
6001 tccccgcttt cccatcccat gctcctcccg gactctatcg tggagccaga gaccccatcc
6061 cagcaagctc actcaggccc ctggctgaca aactcattca cgcactgttt gttcatttaa
6121 cacccactgt gaaccaggca ccagccccca acaaggattc tgaagctgta ggtccttgcc
6181 tctaaggagc ccacagccag tgggggaggc tgacatgaca gacacatagg aaggacatag
6241 taaagatggt ggtcacagag gaggtgacac ttaaagcctt cactggtaga aaagaaaagg

FIG. 15b

```
6301 aggtgttcat tgcagaggaa acagaatgtg caaagactca gaatatggcc tatttaggga
6361 atggctacat acaccatgat tagaggaggc ccagtaaagg gaagggatgg tgagatgcct
6421 gctaggttca ctcactcact tttatttatt tatttatttt tttgacagtc tctctgtcgc
6481 ccaggctgga gtgcagtggt gtgatcttgg gtcactgcaa cttccgcctc ccgggttcaa
6541 gggattctcc tgcctcagct tcctgagtag ctggggttac aggtgtgtgc caccatgccc
6601 agctaatttt ttttttgtatt tttagtagac agggtttcac catgttggtc aggctggtct
6661 caaactcctg gcctcaagtg atccgcctga ctcagcctac caaagtgctg attacaagtg
6721 tgagccaccg tgcccagcca cactcactga ttctttaatg ccagccacac agcacaaagt
6781 tcagagaaat gcctccatca tagcatgtca atatgttcat actcttaggt tcatgatgtt
6841 cttaacatta ggttcataag caaaataaga aaaaagaata ataaataaaa gaagtggcat
6901 gtcaggacct cacctgaaaa gccaaacaca gaatcatgaa ggtgaatgca gaggtgacac
6961 caacacaaag gtgtatatat ggtttcctgt ggggagtatg tacggaggca gcagtgagtg
7021 agactgcaaa cgtcagaagg gcacgggtca ctgagagcct agtatcctag taaagtgggc
7081 tctctccctc tctctccagc ttgtcattga aaaccagtcc accaagcttg ttggttcgca
7141 cagcaagagt acatagagtt tgaaataata cataggattt taagagggag acactgtctc
7201 taaaaaaaaa aacaacagca acaacaaaaa gcaacaacca ttacaatttt atgttccctc
7261 agcattctca gagctgagga atgggagagg actatgggaa ccccccttcat gttccggcct
7321 tcagccatgg ccctggatac atgcactcat ctgtcttaca atgtcattcc cccagGAGGG
7381 CCCGGAAGAA AACAGTGCCT ATGAGCAGTT GCTGTCTCGC TTGGAAGAAA TCGCTGAGGA
7441 AGgtcagttt gttggtctgg ccactaatct ctgtggccta gttcataaag aatcaccctt
7501 tggagcttca ggtctgaggc tggagatggg ctccctccag tgcaggaggg attgaagcat
7561 gagccagcgc tcatcttgat aataaccatg aagctgacag acacagttac ccgcaaacgg
7621 ctgcctacag attgaaaacc aagcaaaaac cgccgggcac ggtggctcac gcctgtaatc
7681 ccagcacttt gggaggccaa ggcaggtgga tcacgaggtc aagagatcaa gaccatcctg
7741 gccaacatgg tgaaacccca tctctactaa aaatacgaaa aaatagccag gcgtggtggc
7801 gggtgcctgt aatcccagct actcgggagg ctgaggcagg agaatggcat gaacccggga
7861 ggcagaagtt gcagtgagcc gagatcgtgc cactgcactc cagcctgggc aacagagcga
7921 gactcttgtc tcaaaaaaaa aaaaaaaaaa gaaaaccaag caaaaaccaa aatgagacaa
7981 aaaaaacaag accaaaaaat ggtgtttgga aattgtcaag gtcaagtctg gagagctaaa
8041 ctttttctga gaactgttta tctttaataa gcatcaaata ttttaacttt gtaaatactt
8101 ttgttggaaa tcgttctctt cttagtcact cttgggtcat tttaaatctc acttactcta
8161 ctagaccttt taggtttctg ctagactagg tagaactctg cctttgcatt tcttgtgtct
8221 gttttgtata gttatcaata ttcatattta tttacaagtt attcagatca ttttttcttt
8281 tctttttttt ttttttttt ttttttacat ctttagtaga gacagggttt caccatattg
8341 gccaggctgc tctcaaactc ctgaccttgt gatccaccag cctcggcctc ccaaagtgct
8401 gggattcatt ttttcttttt aatttgctct gggcttaaac ttgtggccca gcactttatg
8461 atggtacaca gagttaagag tgtagactca gacggtcttt cttctttcct tctcttcctt
8521 cctcccttcc ctcccacctt ccctttctctc cttcctttct ttcttcctct cttgcttcct
8581 caggcctctt ccagttgctc caaagccctg tacttttttt tgagttaacg tcttatggga
8641 agggcctgca cttagtgaag aagtggtctc agagttgagt taccttggct tctgggaggt
8701 gaaactgtat ccctataccc tgaagcttta agggggtgca atgtagatga gaccccaaca
8761 tagatcctct tcacagGCTC AGAGACTCAG GTCCCAGGAC TGGACATATC TGCACTCCTG
8821 CCCTCTGACT TCAGCCGCTA CTTCCAATAT GAGGGGTCTC TGACTACACC GCCCTGTGCC
8881 CAGGGTGTCA TCTGGACTGT GTTTAACCAG ACAGTGATGC TGAGTGCTAA GCAGgtgggc
8941 ctggggtgtg tgtggacaca gtgggtgcgg gggaaagagg atgtaagatg agatgagaaa
9001 caggagaaga aagaaatcaa ggctgggctc tgtggcttac gcctataatc ccaccacgtt
9061 gggaggctga ggtgggagaa tggtttgagc ccaggagttc aagacaaggc ggggcaacat
9121 agtgtgaccc catctctacc aaaaaaaccc caacaaaacc aaaaatagcc gggcatggtg
9181 gtatgcggcc tagtcccagc tactcaagga ggctgaggtg ggaagatcgc ttgattccag
9241 gagtttgaga ctgcagtgag ctatgatccc accactgcct accatctttа ggatacattt
9301 atttatttat aaaagaaatc aagaggctgg atggggaata caggagctgg agggtggagc
9361 cctgaggtgc tggttgtgag ctggcctggg acccttgttt cctgtcatgc catgaaccca
9421 cccacactgt ccactgacct ccctagCTCC ACACCCTCTC TGACACCCTG TGGGGACCTG
9481 GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC TTTGAATGGG CGAGTGATTG
```

FIG. 15c

```
 9541 AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCCTCGGGC TGCTGAGCCA Ggtacagctt
 9601 tgtctggttt ccccccagcc agtagtccct tatcctccca tgtgtgtgcc agtgtctgtc
 9661 attggtggtc acagcccgcc tctcacatct ccttttctc tccagTCCAG CTGAATTCCT
 9721 GCCTGGCTGC TGgtgagtct gcccctcctc ttggtcctga tgccaggaga ctcctcagca
 9781 ccattcagcc ccagggctgc tcaggaccgc ctctgctccc tctccttttc tgcagaacag
 9841 accccaaccc caatattaga gaggcagatc atggtgggga ttcccccatt gtccccagag
 9901 gctaattgat tagaatgaag cttgagaaat ctcccagcat ccctctcgca aaagaatccc
 9961 ccccccttt tttaaagata gggtctcact ctgtttgccc caggctgggg tgttgtggca
10021 cgatcatagc tcactgcagc ctcgaactcc taggctcagg caatcctttc accttagctt
10081 ctcaaagcac tgggactgta ggcatgagcc actgtgcctg gccccaaacg gccctttac
10141 ttggctttta ggaagcaaaa acggtgctta tcttacccct tctcgtgtat ccaccctcat
10201 cccttggctg gcctcttctg gagactgagg cactatgggg ctgcctgaga actcggggca
10261 ggggtggtgg agtgcactga ggcaggtgtt gaggaactct gcagacccct cttccttccc
10321 aaagcagccc tctctgctct ccatcgcagG TGACATCCTA GCCCTGGTTT TTGGCCTCCT
10381 TTTTGCTGTC ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA Ggtattacac
10441 tgacccttc ttcaggcaca agcttccccc acccttgtgg agtcacttca tgcaaagcgc
10501 atgcaaatga gctgctcctg ggccagtttt ctgattagcc tttcctgttg tgtacacaca
10561 gAAGGGGAAC CAAAGGGGGT GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT
10621 AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA
10681 ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA
10741 AATATTTATA ATaaaatatg tgttagtcac ctttgttccc caaatcagaa ggaggtattt
10801 gaatttccta ttactgttat tagcaccaat ttagtggtaa tgcatttatt ctattacagt
10861 tcggcctcct tccacacatc actccaatgt gttgctcc
```

FIG. 15d

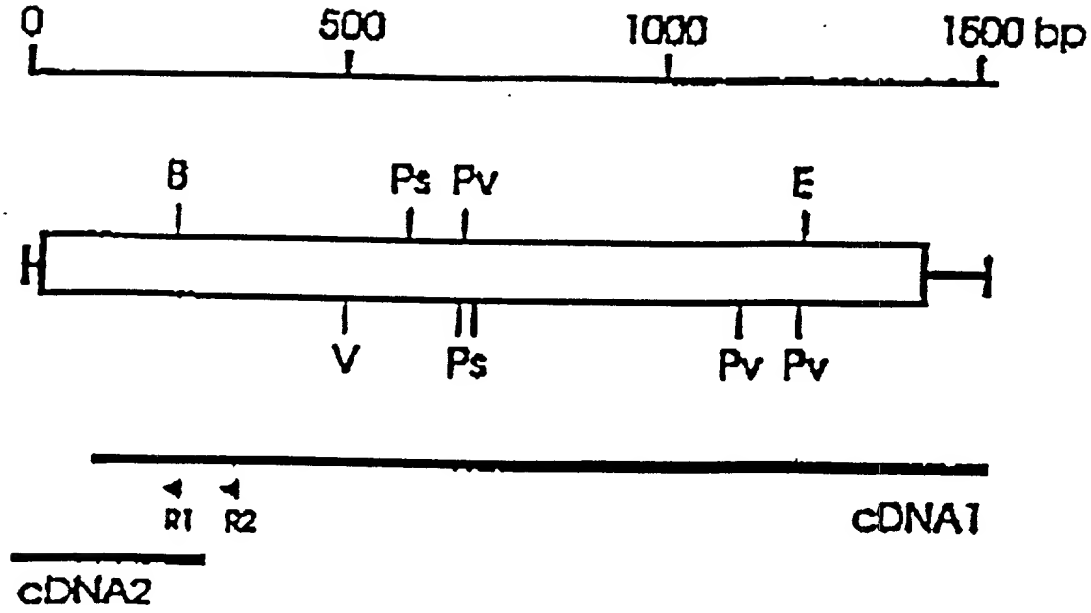


FIG. 16

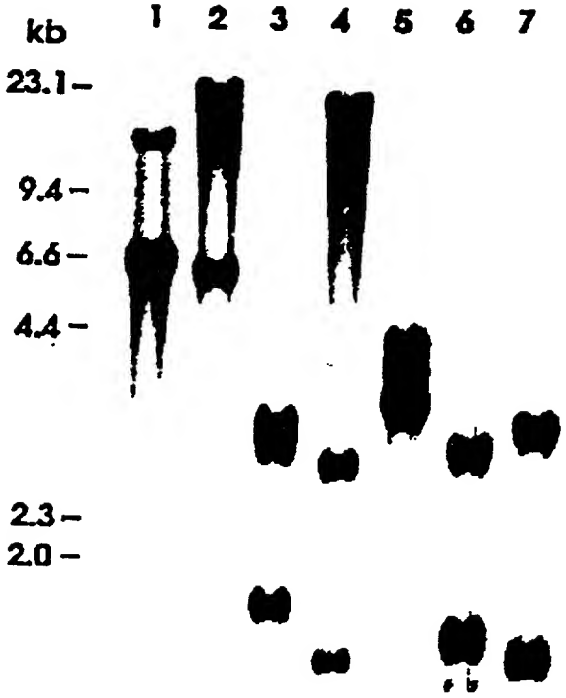


FIG. 17

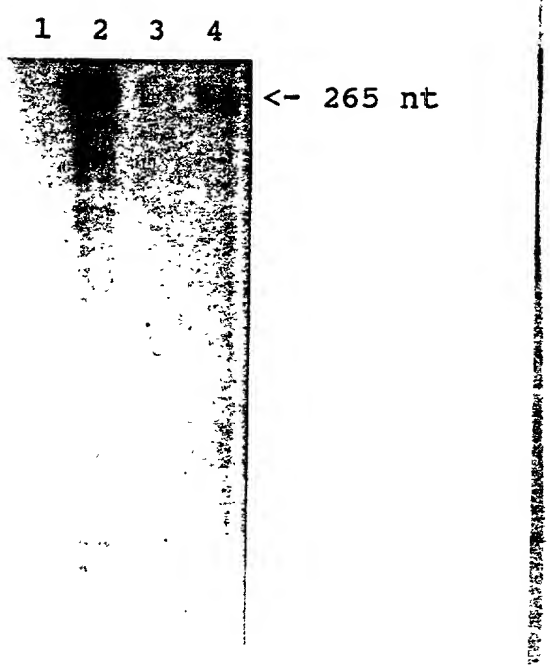


FIG 18a

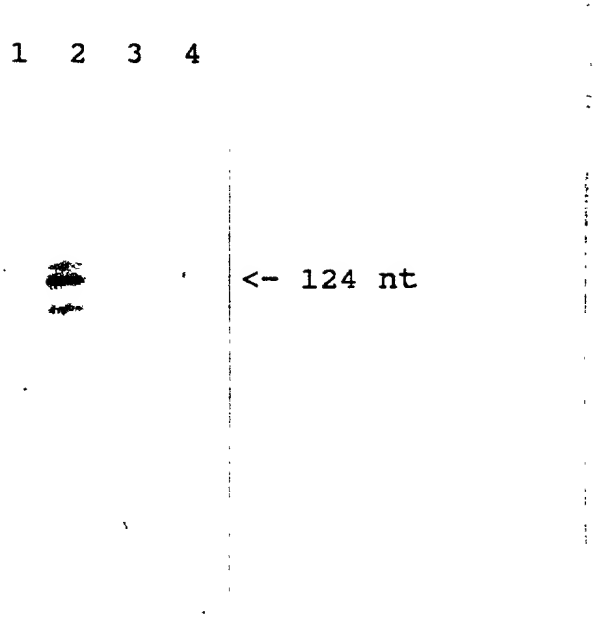


FIG. 18b

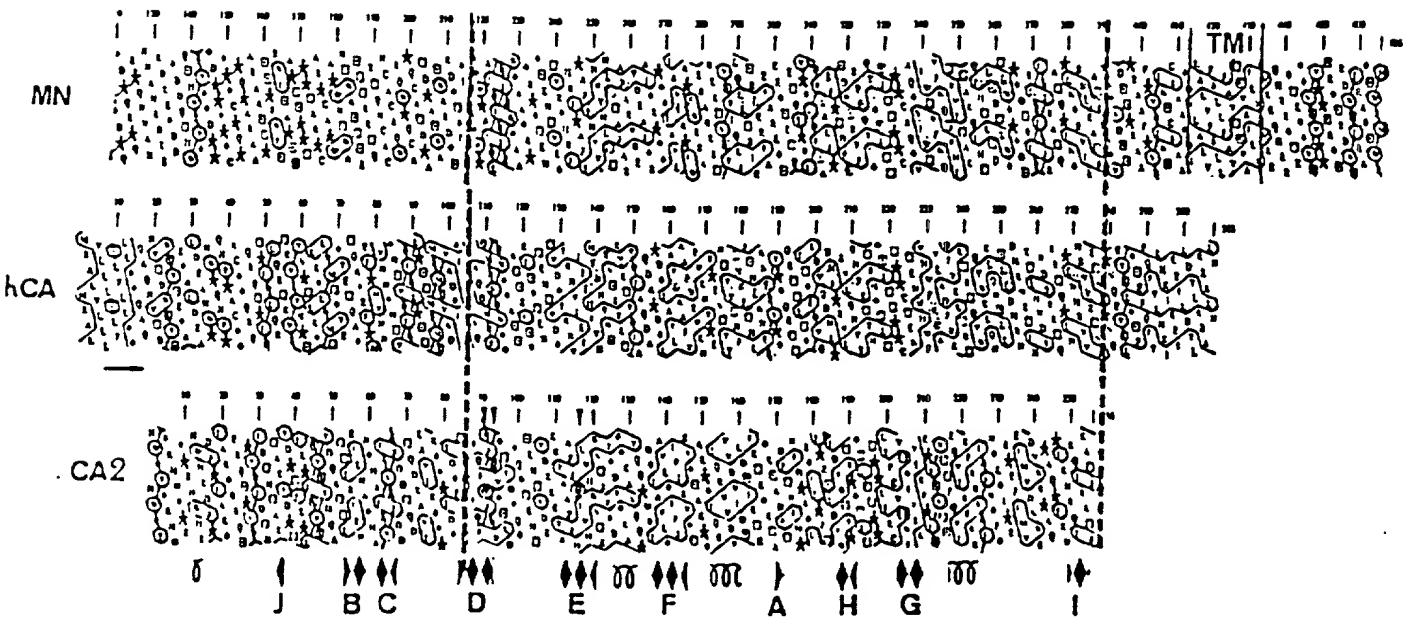


Fig. 19a

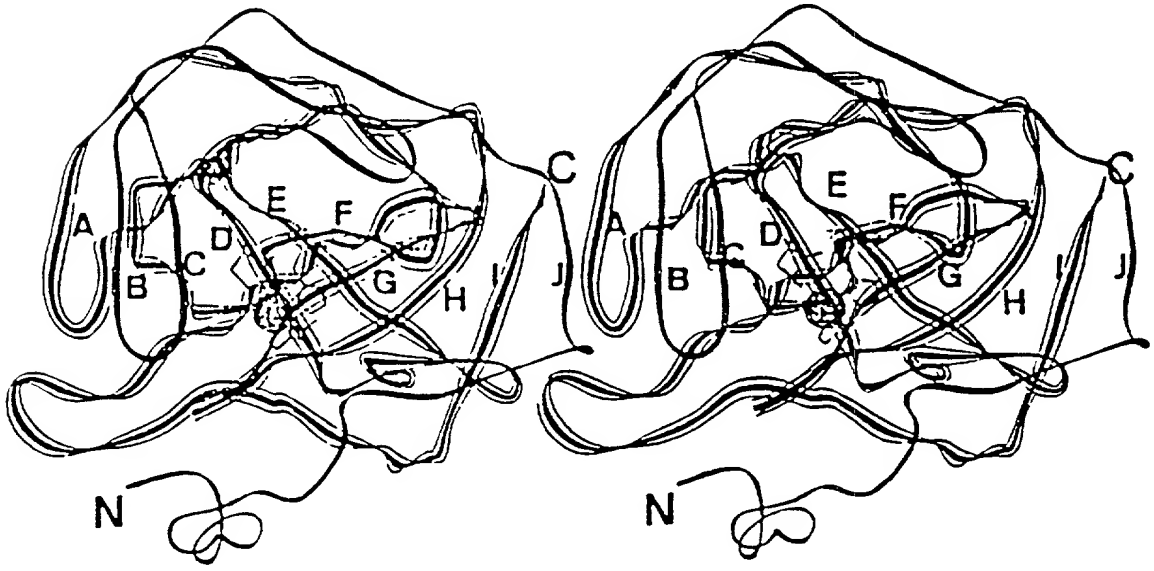


Fig. 19b

5' MN Genomic Region

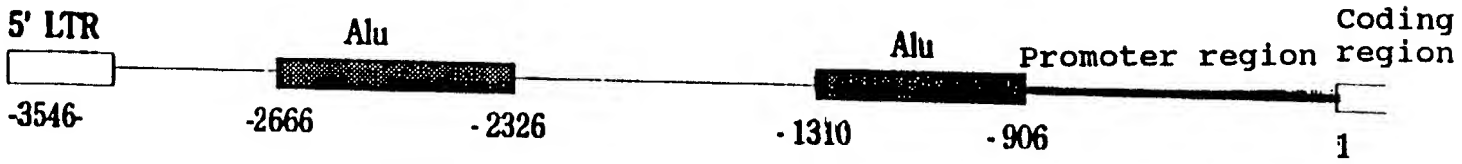


FIG. 20

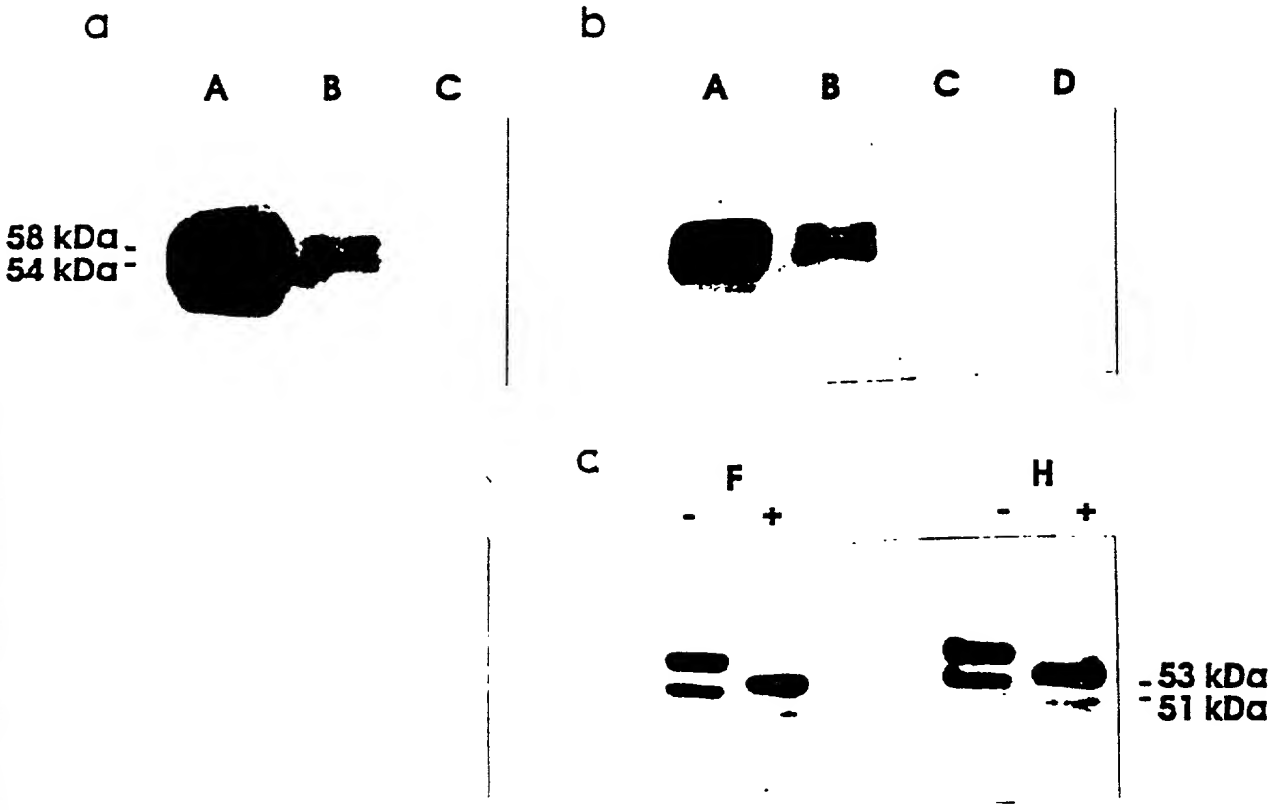


FIG. 21

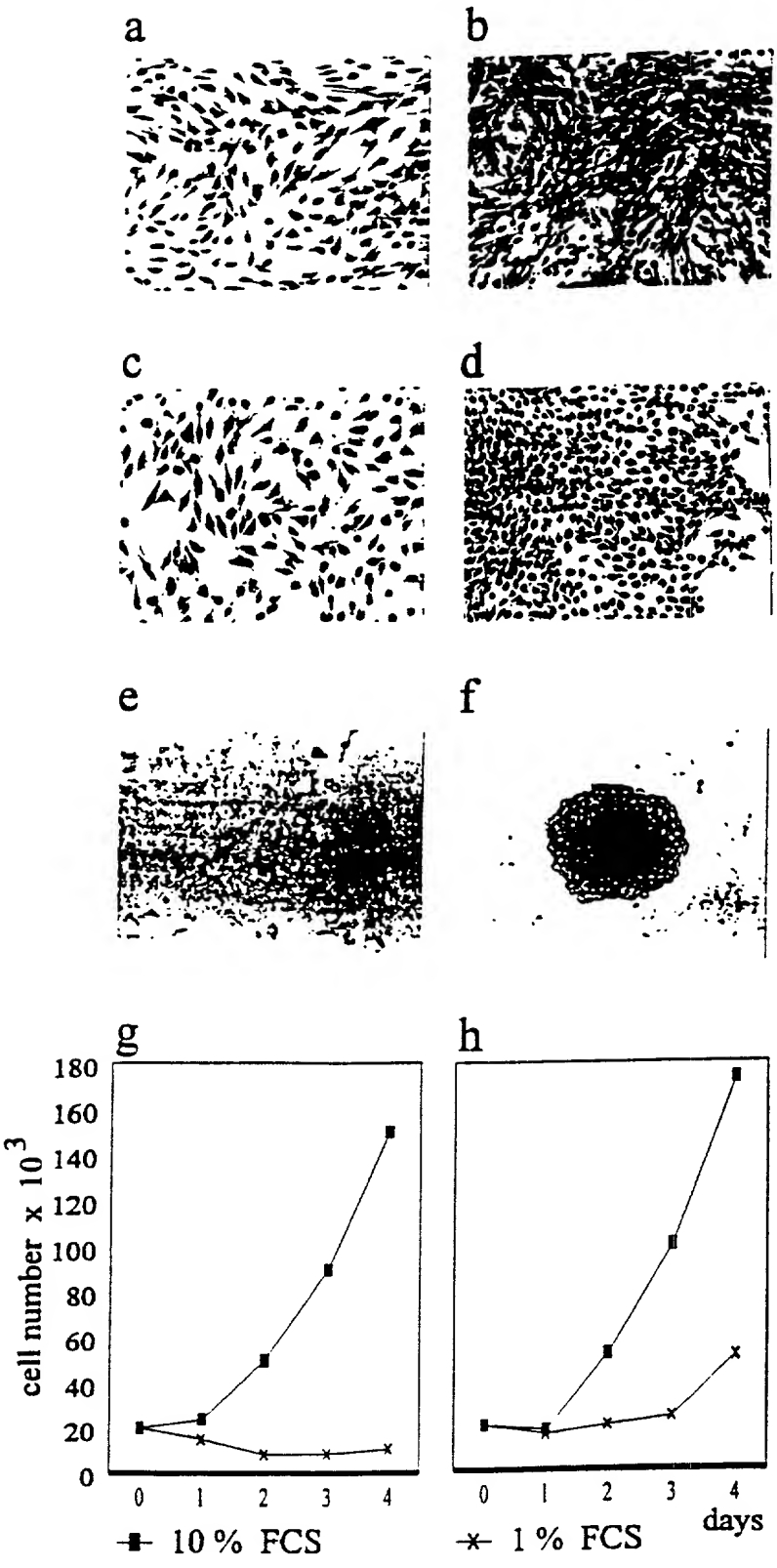
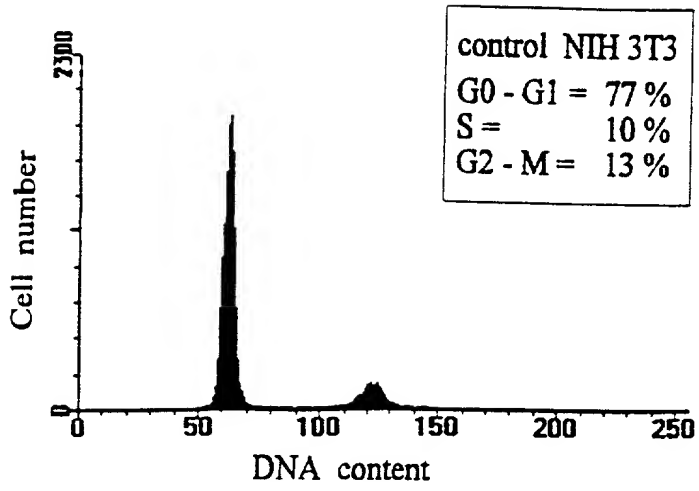
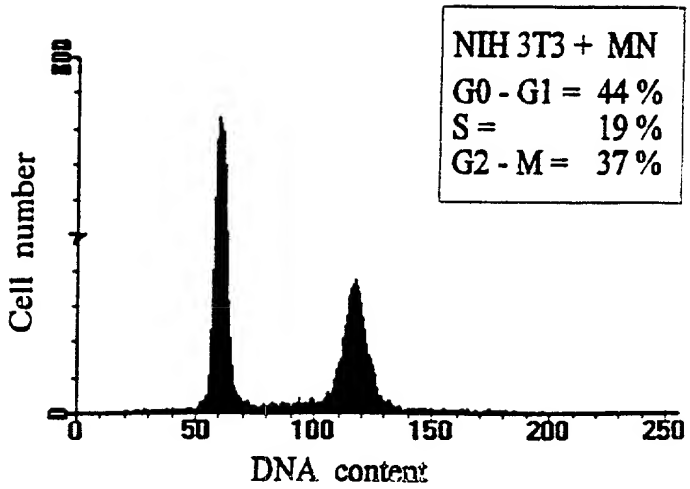

a
b
c
d
e
f
g
h
180
160
140
120
100
80
60
40
20
0
cell number x 10^3
0
1
2
3
4
days
10 % FCS
1 % FCS

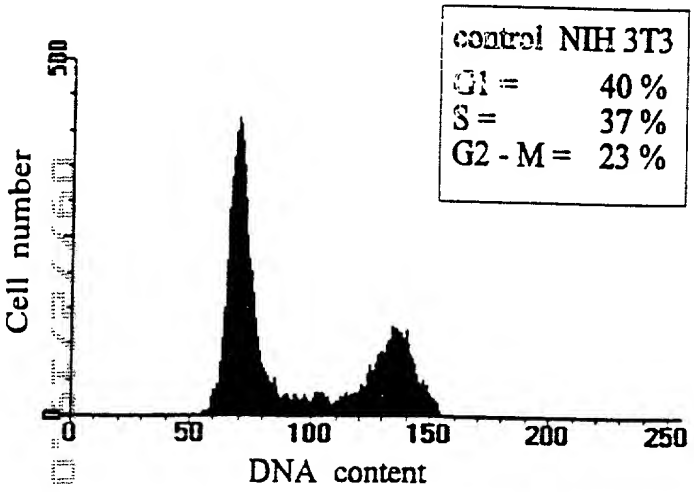
FIG. 22

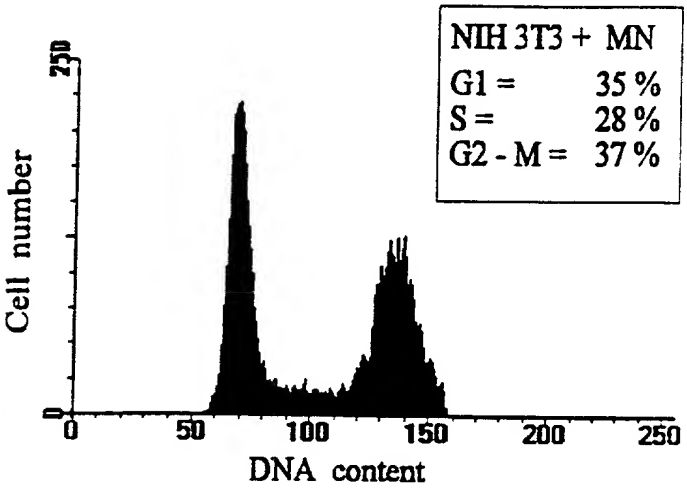
a



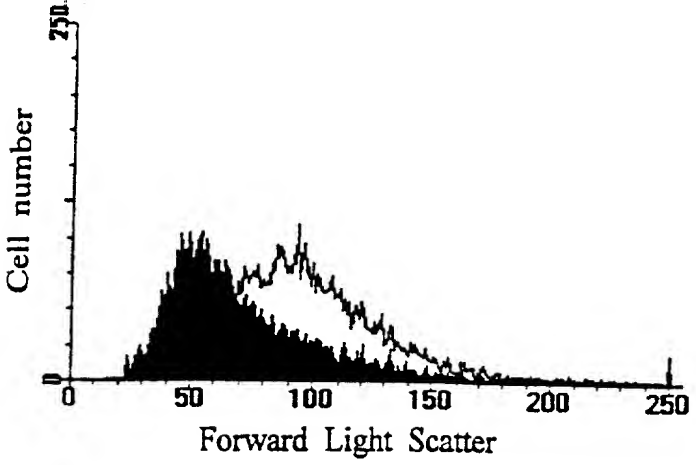


b





c



NIH 3T3 + MN

control NIH 3T3

— Kolmogorov-Smirnov Statistics —
D/s(n) = 19.03
D = 0.36
Channel = 70
Channels 0 - 255
99 % probability of difference

FIG. 23

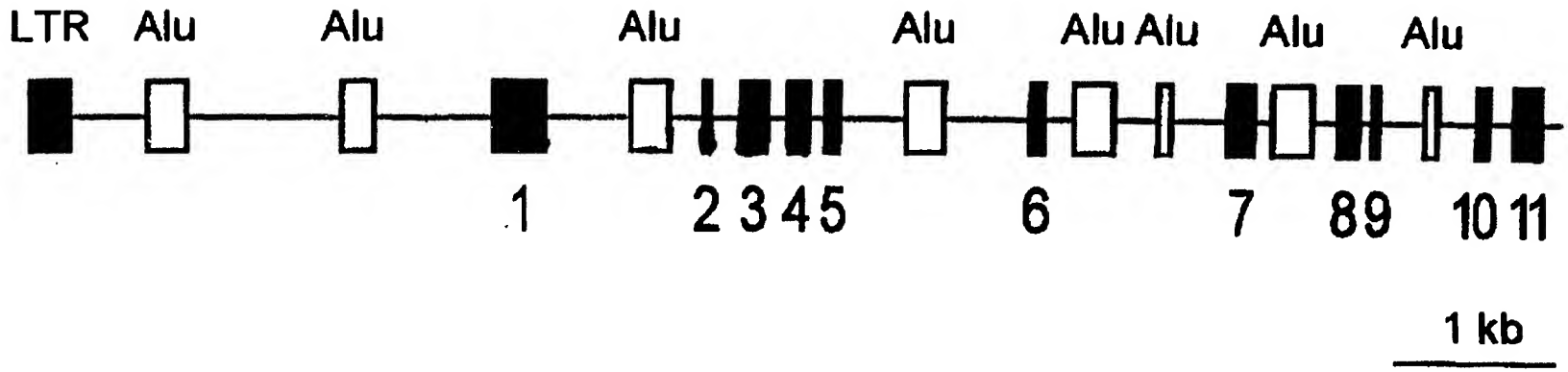


FIG. 24

-506 CTTGCTTTTC ATTCAAGCTC AAGTTTGTCT CCCACATACC CATTACTTAA CTCACCCTCG

-446 GGCTCCCCTA GCAGCCTGCC CTACCTCTTT ACCTGCTTCC TGGTGGAGTC AGGGATGTAT
AP2 AP2

-386 ACATGAGCTG CTTTCCCTCT CAGCCAGAGG ACATGGGGGG CCCCAGCTCC CCTGCCTTTC

-326 CCCTTCTGTG CCTGGAGCTG GGAAGCAGGC CAGGGTTAGC TGAGGCTGGC TGGCAAGCAG

-266 CTGGGTGGTG CCAGGGAGAG CCTGCATAGT GCCAGGTGGT GCCTTGGGTT CCAAGCTAGT
p53

-206 CCATGGCCCC GATAACCTTC TGCCTGTGCA CACACCTGCC CCTCACTCCA CCCCCATCCT
Inr

-146 AGCTTTGGTA TGGGGGAGAG GGCACAGGGC CAGACAAACC TGTGAGACTT TGGCTCCATC
Inr

-86 TCTGCAAAAG GGCGCTCTGT GAGTCAGCCT GCTCCCCTCC AGGCTTGCTC CTCCCCCACC
AP1 p53 AP2
***
...

-26 CAGCTCTCGT TTCCAATGCA CGTACAGCCC GTACACACCG TGTGCTGGGA CACCCCACAG

FIG. 25

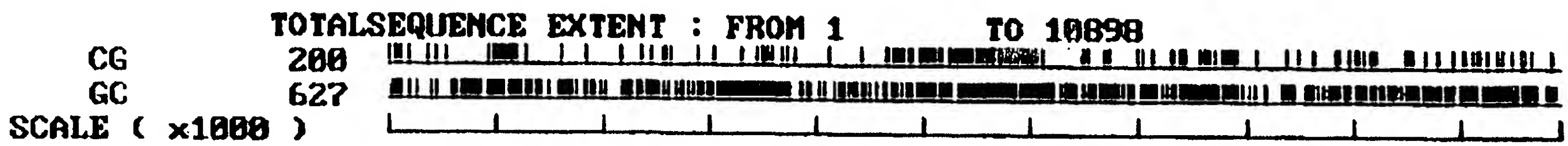

TOTALSEQUENCE EXTENT : FROM 1 TO 10898
CG 200
GC 627
SCALE (x1000)

FIG. 26

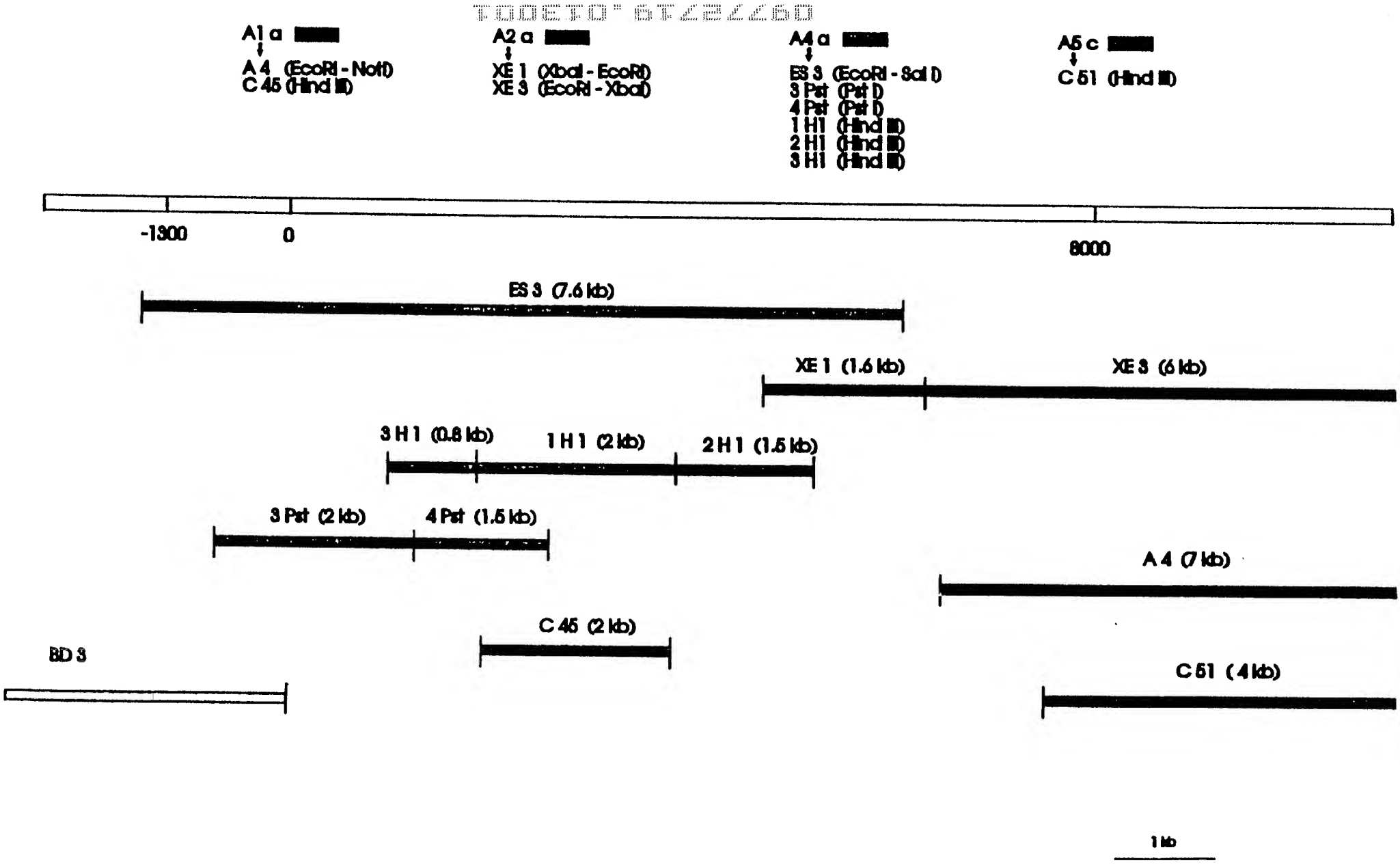

A1 a
A4 (EcoRI - NotI)
C45 (HindIII)
A2 a
XE1 (XbaI - EcoRI)
XE3 (EcoRI - XbaI)
A4 a
ES3 (EcoRI - SalI)
3 Pst (PstI)
4 Pst (PstI)
1 H1 (HindIII)
2 H1 (HindIII)
3 H1 (HindIII)
A5 c
C51 (HindIII)
-1300
0
8000
ES3 (7.6 kb)
XE1 (1.6 kb)
XE3 (6 kb)
3 H1 (0.8 kb)
1 H1 (2 kb)
2 H1 (1.5 kb)
3 Pst (2 kb)
4 Pst (1.5 kb)
A4 (7 kb)
C45 (2 kb)
BD3
C51 (4 kb)
1 kb

FIG. 27

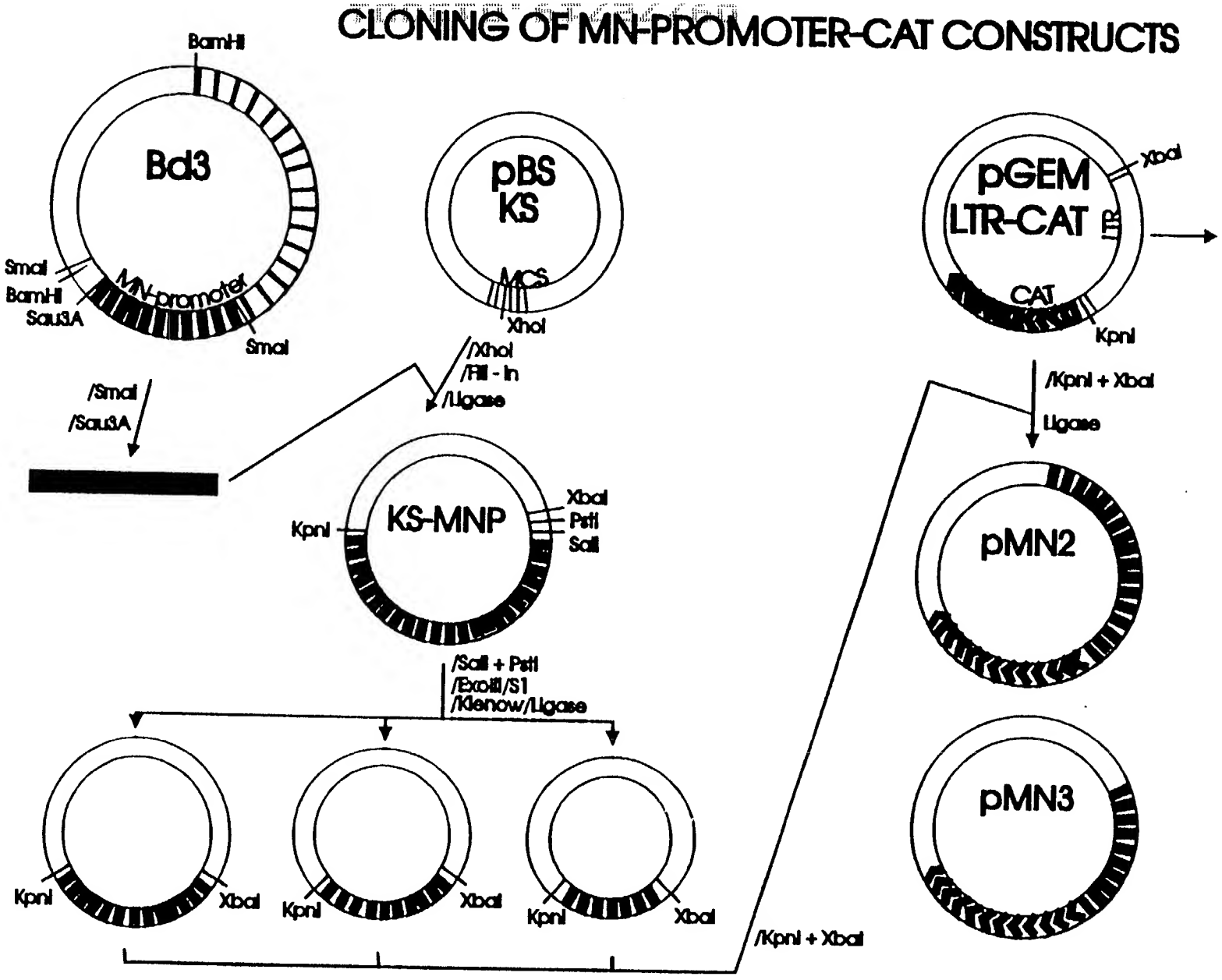

CLONING OF MN-PROMOTER-CAT CONSTRUCTS
BamHI
Bd3
SmaI
BamHI
Sau3A
MN-promoter
SmaI
pBS
KS
MCS
XhoI
pGEM
LTR-CAT
LTR
XbaI
CAT
KpnI
/XhoI
/Fill - In
/Ligase
/SmaI
/Sau3A
/KpnI + XbaI
Ligase
KS-MNP
KpnI
XbaI
PstI
SalI
pMN2
/SalI + PstI
/ExoIII/S1
/Klenow/Ligase
pMN3
KpnI
XbaI
KpnI
XbaI
KpnI
XbaI
/KpnI + XbaI

FIG. 28

STRUCTURE OF MN PROMOTER - CAT CONSTRUCTS

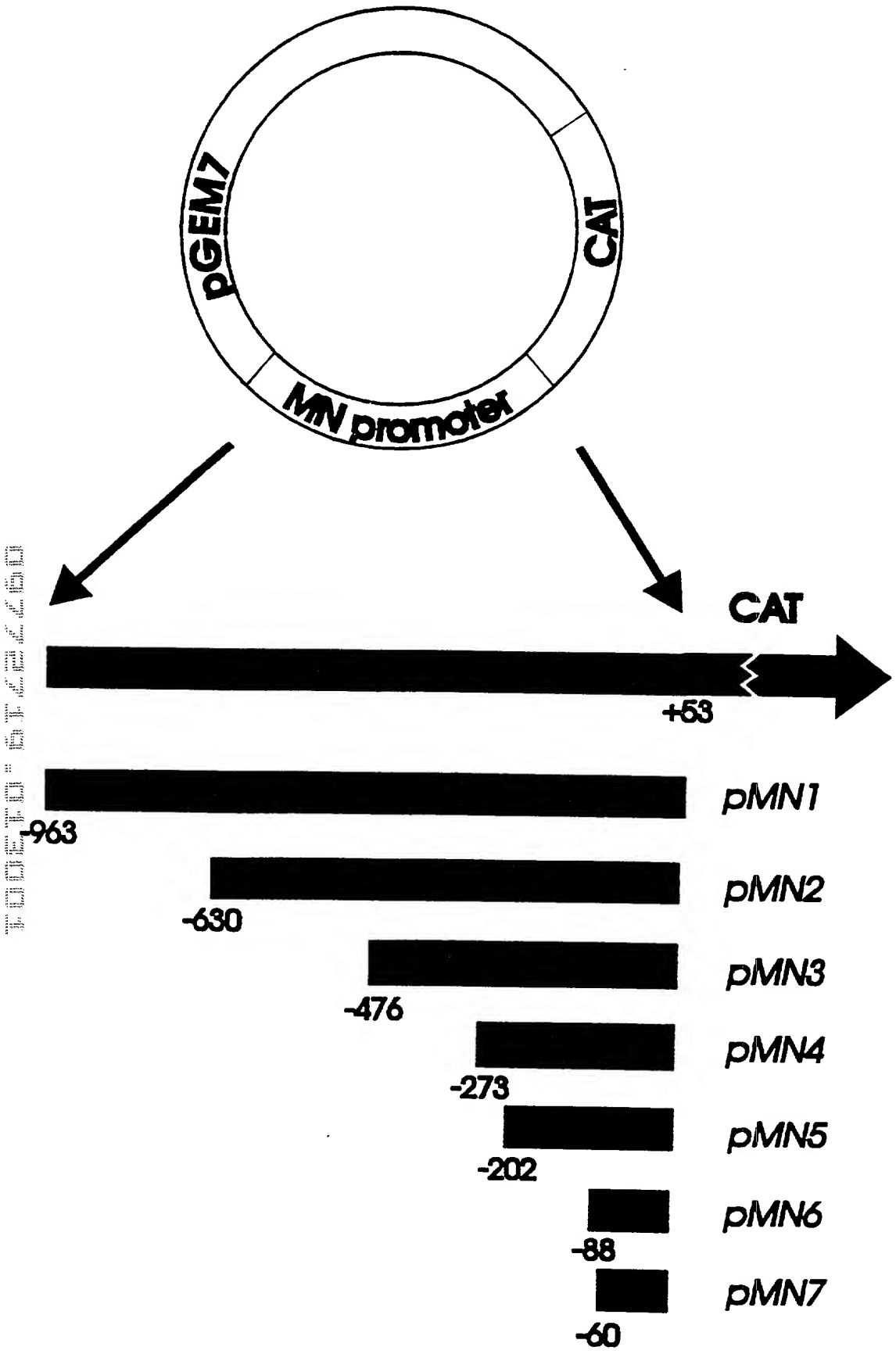


FIG. 29